

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:27:49 ; Search time 69 Seconds
 (without alignments)
 2233.417 Million cell updates/sec

Title: US-10-750-623-21645
 Perfect score: 599.6
 Sequence: 1 tggggtgagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1669160 seqs, 128126992 residues

Total number of hits satisfying chosen parameters: 3338320

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US10_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US09_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS2/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
c 1	35.4	5.9	4037	7	US-11-691-348-343	Sequence 343, App
	2	33	5.5	982	7	Sequence 15217, A
c 3	33	5.5	2171	7	US-11-691-348-266	Sequence 266, App
c 4	33	5.5	2176	7	US-11-691-348-3	Sequence 3, Appli
	5	33	5.5	2581	7	Sequence 15218, A
c 6	33	5.5	3855	7	US-11-691-348-4	Sequence 4, Appli
c 7	33	5.5	4015	7	US-11-691-348-1	Sequence 1, Appli
c 8	33	5.5	4029	7	US-11-691-348-292	Sequence 292, App
c 9	31.8	5.3	2394	7	US-11-514-704-7242	Sequence 7242, Ap

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:27:49 ; Search time 142 Seconds
 (without alignments)
 2233.417 Million cell updates/sec

Title: US-10-750-623-61201
 Perfect score: 1239
 Sequence: 1 ccgactttgcgaccctg.....tcttataatcccttgtat 1239

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1669160 seqs, 128126992 residues

Total number of hits satisfying chosen parameters: 3338320

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US10_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US09_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS2/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	
<hr/>							
c 1	153.2	12.4	15418	7	US-11-710-864-1		Sequence 1, Appli
	2	124.6	10.1	2573	1	US-10-533-069-2374	Sequence 2374, Ap
	3	102.4	8.3	85389	7	US-11-498-489-25	Sequence 25, Appl
	4	86.4	7.0	125958	7	US-11-505-577-26	Sequence 26, Appl
	5	58.8	4.7	42450	7	US-11-730-664-3	Sequence 3, Appli
c 6	40.6	3.3	2181	1	US-10-533-069-1945		Sequence 1945, Ap
	7	39	3.1	1003	1	US-10-438-246-27872	Sequence 27872, A
c 8	37.8	3.1	2596	7	US-11-514-704-12130		Sequence 12130, A
	9	37.4	3.0	2522	7	US-11-514-704-24510	Sequence 24510, A

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:10:22 ; Search time 3606 Seconds
(without alignments)
8154.244 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactttgcgaccctg.....tcttataatcccttgtat 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq:*

17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*

18: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

19: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq:*

20: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11C_PUBCOMB.seq:*

21: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11D_PUBCOMB.seq:*

22: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq:*

23: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11F_PUBCOMB.seq:*

24: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq:*

25: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq:*

26: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq:*

27: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	1239	100.0	1239	11	US-10-750-185-61201	Sequence 61201, A
2	1239	100.0	1239	11	US-10-750-623-61201	Sequence 61201, A
3	1239	100.0	1239	15	US-10-750-622-61201	Sequence 61201, A
4	599.6	48.4	600	11	US-10-750-185-21645	Sequence 21645, A
5	599.6	48.4	600	11	US-10-750-623-21645	Sequence 21645, A
6	599.6	48.4	600	15	US-10-750-622-21645	Sequence 21645, A
7	215.4	17.4	1495	11	US-10-750-185-24940	Sequence 24940, A
8	215.4	17.4	1495	11	US-10-750-623-24940	Sequence 24940, A
9	215.4	17.4	1495	15	US-10-750-622-24940	Sequence 24940, A
10	206.4	16.7	2407	11	US-10-750-185-33843	Sequence 33843, A
11	206.4	16.7	2407	11	US-10-750-623-33843	Sequence 33843, A
12	206.4	16.7	2407	15	US-10-750-622-33843	Sequence 33843, A
c 13	201.4	16.3	2548	11	US-10-750-185-27292	Sequence 27292, A
c 14	201.4	16.3	2548	11	US-10-750-623-27292	Sequence 27292, A
c 15	201.4	16.3	2548	15	US-10-750-622-27292	Sequence 27292, A
16	201	16.2	31296	16	US-10-276-817B-3428	Sequence 3428, Appl
17	201	16.2	32042	3	US-09-728-721-63	Sequence 63, Appl
18	201	16.2	32042	7	US-10-118-984-44	Sequence 44, Appl
19	201	16.2	32042	8	US-10-295-981-63	Sequence 63, Appl
20	201	16.2	32042	11	US-10-843-188-63	Sequence 63, Appl
21	201	16.2	34001	8	US-10-006-883A-15	Sequence 15, Appl
22	201	16.2	39553	23	US-11-033-545-810	Sequence 810, App
23	201	16.2	58111	23	US-11-033-545-673	Sequence 673, App
c 24	201	16.2	68571	8	US-10-401-194-1	Sequence 1, Appli
25	197.2	15.9	305312	11	US-10-995-561-13236	Sequence 13236, A
c 26	193.4	15.6	157090	9	US-10-672-764A-34	Sequence 34, Appl
c 27	193.4	15.6	495635	11	US-10-737-082-12	Sequence 12, Appl
c 28	193.4	15.6	495635	11	US-10-765-790-12	Sequence 12, Appl
c 29	193.4	15.6	705636	11	US-10-737-082-30	Sequence 30, Appl
c 30	193.4	15.6	705636	11	US-10-765-790-30	Sequence 30, Appl
c 31	193.4	15.6	1237661	21	US-11-266-748A-29041	Sequence 29041, A
32	192.4	15.5	2860	11	US-10-481-160-1	Sequence 1, Appli
c 33	191.6	15.5	3285	3	US-09-854-867-425	Sequence 425, App
c 34	191.6	15.5	3285	11	US-10-786-970A-425	Sequence 425, App
35	190.8	15.4	413	3	US-09-960-352-10758	Sequence 10758, A
c 36	188.2	15.2	1000	21	US-11-266-748A-197063	Sequence 197063,
37	188	15.2	466	4	US-09-925-065A-319604	Sequence 319604,
38	188	15.2	466	5	US-09-925-065A-319604	Sequence 319604,
39	188	15.2	466	13	US-10-301-480-394352	Sequence 394352,
40	188	15.2	466	13	US-10-301-480-1007761	Sequence 1007761,
41	188	15.2	558	4	US-09-925-065A-659902	Sequence 659902,
42	188	15.2	558	5	US-09-925-065A-659902	Sequence 659902,
43	186.8	15.1	558	4	US-09-925-065A-659901	Sequence 659901,
44	186.8	15.1	558	5	US-09-925-065A-659901	Sequence 659901,
45	185.2	14.9	102115	16	US-10-990-328-97355	Sequence 97355, A

rnphm-21645

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:10:22 ; Search time 1746 Seconds
(without alignments)
8154.244 Million cell updates/sec

Title: US-10-750-623-21645
Perfect score: 599.6
Sequence: 1 tggggtgagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq:*

17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*

18: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

19: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq:*

20: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11C_PUBCOMB.seq:*

21: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11D_PUBCOMB.seq:*

22: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq:*

23: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11F_PUBCOMB.seq:*

24: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq:*

25: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq:*

26: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq:*

27: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query					Description
			Match	Length	DB	ID		
	1	599.6	100.0	600	11	US-10-750-185-21645		Sequence 21645, A
	2	599.6	100.0	600	11	US-10-750-623-21645		Sequence 21645, A
	3	599.6	100.0	600	15	US-10-750-622-21645		Sequence 21645, A
	4	599.6	100.0	1239	11	US-10-750-185-61201		Sequence 61201, A
	5	599.6	100.0	1239	11	US-10-750-623-61201		Sequence 61201, A
	6	599.6	100.0	1239	15	US-10-750-622-61201		Sequence 61201, A
	7	202.2	33.7	31296	16	US-10-276-817B-3428		Sequence 3428, Appl
	8	202.2	33.7	32042	3	US-09-728-721-63		Sequence 63, Appl
	9	202.2	33.7	32042	7	US-10-118-984-44		Sequence 44, Appl
	10	202.2	33.7	32042	8	US-10-295-981-63		Sequence 63, Appl
	11	202.2	33.7	32042	11	US-10-843-188-63		Sequence 63, Appl
	12	202.2	33.7	34001	8	US-10-006-883A-15		Sequence 15, Appl
	13	202.2	33.7	39553	23	US-11-033-545-810		Sequence 810, App
	14	202.2	33.7	58111	23	US-11-033-545-673		Sequence 673, App
c	15	202.2	33.7	68571	8	US-10-401-194-1		Sequence 1, Appli
	16	72	12.0	3080	3	US-09-728-721-25		Sequence 25, Appl
	17	72	12.0	3080	7	US-10-105-931-25		Sequence 25, Appl
	18	72	12.0	3080	7	US-10-118-984-25		Sequence 25, Appl
	19	72	12.0	3080	8	US-10-006-883A-94		Sequence 94, Appl
	20	72	12.0	3080	8	US-10-295-981-25		Sequence 25, Appl
	21	72	12.0	3080	11	US-10-843-188-25		Sequence 25, Appl
	22	72	12.0	4608	11	US-10-956-157-4599		Sequence 4599, Ap
	23	72	12.0	4610	8	US-10-006-883A-11		Sequence 11, Appl
	24	72	12.0	4610	16	US-10-917-503-18312		Sequence 18312, A
	25	72	12.0	4613	26	US-11-443-428A-443967		Sequence 443967,
	26	69.4	11.6	536	3	US-09-764-855-30.		Sequence 30, Appl
	27	69.4	11.6	536	7	US-10-072-349-30		Sequence 30, Appl
	28	69.4	11.6	2224	26	US-11-443-428A-443971		Sequence 443971,
	29	69.4	11.6	2614	26	US-11-443-428A-443977		Sequence 443977,
	30	69.4	11.6	2859	3	US-09-728-721-9		Sequence 9, Appli
	31	69.4	11.6	2859	7	US-10-105-931-9		Sequence 9, Appli
	32	69.4	11.6	2859	7	US-10-118-984-9		Sequence 9, Appli
	33	69.4	11.6	2859	8	US-10-295-981-9		Sequence 9, Appli
	34	69.4	11.6	2859	11	US-10-843-188-9		Sequence 9, Appli
	35	69.4	11.6	2859	11	US-10-966-846-3		Sequence 3, Appli
	36	69.4	11.6	3382	3	US-09-728-721-7		Sequence 7, Appli
	37	69.4	11.6	3382	7	US-10-105-931-7		Sequence 7, Appli
	38	69.4	11.6	3382	7	US-10-118-984-7		Sequence 7, Appli
	39	69.4	11.6	3382	8	US-10-295-981-7		Sequence 7, Appli
	40	69.4	11.6	3382	11	US-10-843-188-7		Sequence 7, Appli
	41	69.4	11.6	3382	11	US-10-966-846-1		Sequence 1, Appli
	42	69.4	11.6	3589	26	US-11-443-428A-443975		Sequence 443975,
	43	69.4	11.6	3616	26	US-11-443-428A-443972		Sequence 443972,
	44	69.4	11.6	3789	7	US-10-013-477-10		Sequence 10, Appli
	45	69.4	11.6	3789	16	US-10-100-683-4255		Sequence 4255, Ap

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:58:39 ; Search time 351 Seconds
 (without alignments)
 6408.357 Million cell updates/sec

Title: US-10-750-623-21645
 Perfect score: 599.6
 Sequence: 1 tggggtgagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:
 1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*
 6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
 7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*
 8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq:*
 9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*
 10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*
 11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	202.2	33.7	32042	3	US-09-245-281-44	Sequence 44, Appl
2	202.2	33.7	32042	3	US-09-340-620A-63	Sequence 63, Appl
3	202.2	33.7	32042	3	US-09-728-721-63	Sequence 63, Appl
4	202.2	33.7	32042	5	US-10-118-984-44	Sequence 44, Appl
5	202.2	33.7	39553	3	US-09-949-002-810	Sequence 810, App
6	202.2	33.7	58111	3	US-09-949-002-673	Sequence 673, App

^

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:58:39 ; Search time 724 Seconds
 (without alignments)
 6408.357 Million cell updates/sec

Title: US-10-750-623-61201
 Perfect score: 1239
 Sequence: 1 ccgactttgcgaccctg.....tcttataatcccttgtat 1239

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*

6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*

7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*

8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq:*

9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*

10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*

11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	201	16.2	32042	3	US-09-245-281-44	Sequence 44, Appl
2	201	16.2	32042	3	US-09-340-620A-63	Sequence 63, Appl
3	201	16.2	32042	3	US-09-728-721-63	Sequence 63, Appl
4	201	16.2	32042	5	US-10-118-984-44	Sequence 44, Appl
5	201	16.2	39553	3	US-09-949-002-810	Sequence 810, App
6	201	16.2	58111	3	US-09-949-002-673	Sequence 673, App

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:26 ; Search time 4064 Seconds
(without alignments)
18914.697 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactttgcgaccctg.....tcttataatcccttgtt 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_est13:
12: gb_est12:
13: gb_est11:
14: gb_est10:
15: gb_gss1:
16: gb_gss2:
17: gb_gss3:
18: gb_gss4:
19: gb_gss5:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
	249	20.1	605	19	CT185030	CT185030 Sus scrof
c	249	20.1	864	19	CT265370	CT265370 Sus scrof
c	247.6	20.0	814	19	CT438819	CT438819 Sus scrof
	246	19.9	779	19	CT372765	CT372765 Sus scrof
c	246	19.9	885	19	CT425116	CT425116 Sus scrof
	244.4	19.7	829	19	CT102470	CT102470 Sus scrof
	242.6	19.6	808	19	CT445831	CT445831 Sus scrof
c	241.4	19.5	722	19	CT267357	CT267357 Sus scrof
	241.4	19.5	752	17	CL373561	CL373561 RPCI44_45
	241.4	19.5	811	19	CT440825	CT440825 Sus scrof
	239.6	19.3	871	19	CT473538	CT473538 Sus scrof
	239.6	19.3	872	19	CT316901	CT316901 Sus scrof
c	239.6	19.3	915	19	CT224928	CT224928 Sus scrof
	239	19.3	917	19	CT379372	CT379372 Sus scrof
	238.8	19.3	831	19	CT380271	CT380271 Sus scrof
	238.6	19.3	841	19	CT465534	CT465534 Sus scrof
	238	19.2	714	19	CT100278	CT100278 Sus scrof
	238	19.2	801	19	CT475998	CT475998 Sus scrof
	238	19.2	806	19	CT320919	CT320919 Sus scrof
	238	19.2	809	19	CT248002	CT248002 Sus scrof
	238	19.2	812	19	CT396728	CT396728 Sus scrof
	238	19.2	824	19	CT442943	CT442943 Sus scrof
c	238	19.2	837	19	CT200491	CT200491 Sus scrof
	238	19.2	839	19	CT264675	CT264675 Sus scrof
	238	19.2	882	19	CT467508	CT467508 Sus scrof
	238	19.2	884	19	CT373719	CT373719 Sus scrof
	236.4	19.1	741	19	CT335577	CT335577 Sus scrof
	236.4	19.1	760	19	CT452143	CT452143 Sus scrof
	236.4	19.1	792	19	CT269294	CT269294 Sus scrof
c	236.4	19.1	804	19	CT285571	CT285571 Sus scrof
	236.4	19.1	809	19	CT313761	CT313761 Sus scrof
	236.4	19.1	829	19	CT293886	CT293886 Sus scrof
	236.4	19.1	830	19	CT130537	CT130537 Sus scrof
c	236.4	19.1	860	19	CT350038	CT350038 Sus scrof
c	236.4	19.1	873	19	CT244745	CT244745 Sus scrof
	236.4	19.1	882	19	CT329087	CT329087 Sus scrof
c	236.4	19.1	891	19	CT447279	CT447279 Sus scrof
	236.4	19.1	900	19	CT130475	CT130475 Sus scrof
c	235.8	19.0	894	19	CT399477	CT399477 Sus scrof
	235	19.0	793	19	CT369120	CT369120 Sus scrof
	234.8	19.0	695	17	CL323492	CL323492 RPCI44_45
	234.8	19.0	745	17	CL382186	CL382186 RPCI44_32
	234.8	19.0	781	19	CT293222	CT293222 Sus scrof
	234.8	19.0	782	19	CT410916	CT410916 Sus scrof
	234.8	19.0	785	19	CT326765	CT326765 Sus scrof

ALIGNMENTS

RESULT 1

CT185030

LOCUS CT185030 605 bp DNA linear GSS 02-NOV-2005

DEFINITION Sus scrofa genomic clone CH242-113I11, genomic survey sequence.

ACCESSION CT185030

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:26 ; Search time 1968 Seconds
(without alignments)
18914.697 Million cell updates/sec

Title: US-10-750-623-21645

Perfect score: 599.6

Sequence: 1 tgggtgagggaggcaaaca.....atacgacctgctctgtac 600

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

7: gb_est2:*

8: gb_est7:*

 9: gb_est8:*

 10: gb_est9:*

 11: gb_est13:*

 12: gb_est12:*

 13: gb_est11:*

 14: gb_est10:*

 15: gb_gss1:*

 16: gb_gss2:*

 17: gb_gss3:*

 18: gb_gss4:*

 19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
--------	-------	-----	-------	-------	--------	----	----	-------------

1	188.6	31.5	3124	6	BC020114			BC020114 Homo sapi
2	154.2	25.7	644	17	CL371847			CL371847 RPCI44_30
3	85.8	14.3	823	10	CO886987			CO886987 BovGen_15
4	85.8	14.3	1133	12	DV793189			DV793189 Hw_loin_E
5	75	12.5	542	2	BE633255			BE633255 uv74g04.y
6	72	12.0	891	8	CF618769			CF618769 AGENCOURT
7	72	12.0	907	8	CF618768			CF618768 AGENCOURT
8	69.4	11.6	2862	19	AY418482			AY418482 Homo sapi
9	68.4	11.4	697	4	BP151920			BP151920 BP151920
c 10	66.4	11.1	509	4	BQ327671			BQ327671 MR1-RT003
11	66	11.0	1134	3	BM549076			BM549076 AGENCOURT
12	61	10.2	849	12	DV814288			DV814288 LB01712.C
13	58.8	9.8	773	1	AI561834			AI561834 vk33g03.y
14	58.6	9.8	932	4	BQ900609			BQ900609 AGENCOURT
15	58.2	9.7	433	1	AI607231			AI607231 vo63c02.y

7e-61201

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:12 ; Search time 8383 Seconds
(without alignments)
10216.382 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactttgcgaccctg.....tcttataatcccttgtat 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_env:
2: gb_pat:
3: gb_ph:
4: gb_pl:
5: gb_pr:
6: gb_ro:
7: gb_sts:
8: gb_sy:
9: gb_un:
10: gb_vi:
11: gb_ov:
12: gb_htg:
13: gb_in:
14: gb_om:
15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description	
No.	Score	Match	Length	DB	ID	
1	1190.8	96.1	332533	12	AC152664	AC152664 Bos tauru
c	1186	95.7	188320	12	AC092085	AC092085 Bos tauru

rgl-21645

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:12 ; Search time 4059 Seconds
(without alignments)
10216.382 Million cell updates/sec

Title: US-10-750-623-21645

Perfect score: 599.6

Sequence: 1 tggggtgagggaggcaaaca.....atacgacacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_env:
2: gb_pat:
3: gb_ph:
4: gb_pl:
5: gb_pr:
6: gb_ro:
7: gb_sts:
8: gb_sy:
9: gb_un:
10: gb_vi:
11: gb_ov:
12: gb_htg:
13: gb_in:
14: gb_om:
15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	587.6	98.0	188320	12	AC092085	AC092085 Bos tauru
c 2	587.6	98.0	211084	12	AC092084	AC092084 Bos tauru

1ng-61201

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:43:54 ; Search time 999 Seconds
(without alignments)
9189.503 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactttgcgaccctg.....tcttataatcccttgtat 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	201	16.2	32042	2	AAZ09252	Aaz09252 Human CAR

rng-21645

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:43:54 ; Search time 484 Seconds
(without alignments)
9189.503 Million cell updates/sec

Title: US-10-750-623-21645
Perfect score: 599.6
Sequence: 1 tggggtagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	202.2	33.7	32042	2	AAZ09252	Aaz09252 Human CAR